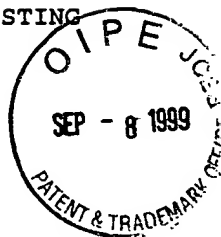


SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Behan, Dominic P.
Chalmers, Derek T.
- (ii) TITLE OF INVENTION: A Method of Identifying Modulators of
Cell Surface Membrane Receptors Useful in the Treatment of
Disease
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arena Pharmaceuticals, Inc.
 - (B) STREET: 6166 Nancy Ridge Drive
 - (C) CITY: San Diego
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 92121
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 14-APR-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Burgoon, Richard P.
 - (B) REGISTRATION NUMBER: 34,787
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-453-7200
 - (B) TELEFAX: 619-453-7210

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Tyr Ala Gly Ile Leu Ser Tyr Arg Val Gly Phe Phe Leu Phe Ile
 1 5 10 15

Leu Val Val Ala Ala Val Thr Leu Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Gln Leu Pro Tyr Asp His
 1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Cys Ser Arg Glu Lys Lys Ala Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser
 1 5 10 15
 Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly
 20 25 30
 Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Ser Arg Glu
 35 40 45
 Lys Lys Ala Ala Lys Thr
 50

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: one-of(7)
 (D) OTHER INFORMATION: /product= "OTHER"

/label= Xaa

/note= "Xaa is an amino acid other than Ala. Most preferably,
 Xaa is Glu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Arg Glu Lys Lys Ala Xaa Lys Thr Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: one-of(69)
 (D) OTHER INFORMATION: /product= "OTHER"

/label= Xaa

/note= "Xaa is an amino acid other than Ala. Most preferably,
 Xaa is Glu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Val Tyr Ile Val Ala Lys Arg Thr Thr Lys Asn Leu Glu Ala Gly
 1 5 10 15

Val Met Lys Glu Met Ser Asn Ser Lys Glu Leu Thr Leu Arg Ile His
 20 25 30

Ser Lys Asn Phe His Glu Asp Thr Leu Ser Ser Thr Lys Ala Lys Gly
 35 40 45

His Asn Pro Arg Ser Ser Ile Ala Val Lys Leu Phe Lys Phe Ser Arg
 50 55 60

Glu Lys Lys Ala Xaa Lys Thr Leu
 65 70

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Leu Asp Gly Leu Thr Thr Cys Gly Val Val Tyr Pro Leu Ser Lys
 1 5 10 15

Asn His Leu Val Val Leu
 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Arg Ile Val Cys Arg His Ala Gln Gln Ile Ala Leu Gln Arg His
 1 5 10 15

Leu Leu Pro Ala Ser His Tyr Val Ala Thr Arg Lys Gly

20

25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Tyr Ile Thr Val Arg Asn Pro Gln Tyr Asn Pro Gly Asp Lys Gly Thr
 1 5 10 15

Lys Ile Ile Lys Arg
 20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Tyr Ile Thr Val Arg Asn Pro Gln Tyr Asn Pro Gly Asp Lys Cys Thr
 1 5 10 15

Lys Ile Ile Lys Arg
 20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val Thr Ile Leu

1

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Leu Ile Thr Arg Thr Val Lys Lys

1

5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Thr Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Ala Tyr

1

5

10

15

Thr Leu Thr Val Ile Thr Leu Glu

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Leu Leu Val Leu Phe Tyr Pro Leu Asn Ser Tyr Ala Asn Pro Phe
 1 5 10 15

Leu Tyr Ala Ile Phe Thr Lys Ala
 20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 - (B) LOCATION: one-of(1)
 - (D) OTHER INFORMATION: /product= "OTHER"
- /label= Xaa
 /note= "Xaa is normally either Glu or Asp."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Xaa Arg Tyr
 1

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Lys Lys Ala Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: one-of(1)
- (D) OTHER INFORMATION: /product= "OTHER"

/label= Xaa

/note= "First Xaa can be any amino acid, preferably Gly, Ala, or Lys."

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: one-of(2, 3)
- (D) OTHER INFORMATION: /product= "OTHER"

/label= Xaa

/note= "Second and third Xaa denote a basic amino acid"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: one-of(4)
- (D) OTHER INFORMATION: /product= "OTHER"

/label= Xaa

/note= "Fourth Xaa denotes a hydrophobic amino acid"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: one-of(5)
- (D) OTHER INFORMATION: /product= "OTHER"

/label= Xaa

/note= "Fifth Xaa denotes any amino acid, preferably Lys, Arg, Glu, or a hydrophobic amino acid with a differing side chain to the original hydrophobic amino acid in that position."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: one-of(9)
- (D) OTHER INFORMATION: /product= "OTHER"

/label= Xaa

/note= "Xaa is Glu, Asp, Gln, His or Lys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val	Tyr	Ala	Gly	Ile	Leu	Ser	Tyr	Xaa	Gly	Phe	Phe	Leu	Phe	Ile	Leu
1				5					10					15	
Val Val Ala Ala Val Thr Leu Cys															
20															

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Val	Thr	Phe	Ile	Ile	Ala	Thr	Val	Glu	Gly	Val	Leu	Leu	Phe	Leu	Ile
1				5					10					15	
Leu Val Val Val Val Gly Ile Leu Ile															
20 25															

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gln	Leu	Pro	Tyr
1			

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTGGTCCTGC ACTTTGCTGC

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCATCACAT AGGTCCGTGT CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACCAGAAAGG GTGTGGGTAC ACTG

24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGAACGAAAG GGCACCTTTGG

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTGCCTCGG GATTATTTAG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCCTATTAGC AGGAACATGG GTG

23

SEQUENCE LISTING

<110> Arena Pharmaceuticals, Inc.

<120> A Method of Identifying Modulators of Cell Surface
Membrane Receptors Useful in the Treatment of Disease

<130> 3086-4

<140> 09/060,188

<141> 1998-04-14

<160> 29

<170> PatentIn Ver. 2.1

<210> 1

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<212> PRT

<213> Homo Sapien

<400> 1

Val	Tyr	Ala	Gly	Ile	Leu	Ser	Tyr	Arg	Val	Gly	Phe	Phe	Leu	Phe	Ile
1				5					10				15		

Leu	Val	Val	Ala	Ala	Val	Thr	Leu	Cys
			20				25	

<210> 2

<211> 7

<212> PRT

<213> Homo Sapien

<400> 2

Thr	Gln	Leu	Pro	Tyr	Asp	His
1				5		

<210> 3

<211> 9

<212> PRT

<213> Homo Sapien

<400> 3

Phe	Cys	Ser	Arg	Glu	Lys	Lys	Ala	Ala
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<210> 4

<211> 54

<212> PRT

<213> Homo Sapien

<400> 4

Arg	Val	Phe	Gln	Glu	Ala	Lys	Arg	Gln	Leu	Gln	Lys	Ile	Asp	Lys	Ser
1				5					10				15		

Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly
20 25 30

Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Ser Arg Glu
35 40 45

Lys Lys Ala Ala Lys Thr
50

<210> 5
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<212> PRT
<213> Homo Sapien

<220>
<223> Xaa is an amino acid other than Ala. Most
preferably, Xaa is Glu.

<400> 5
Ser Arg Glu Lys Lys Ala Xaa Lys Thr Leu
1 5 10

<210> 6
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<212> PRT
<213> Homo Sapien

<220>
<223> Xaa is an amino acid other than Ala. Most
preferably, Xaa is Glu.

<400> 6
Arg Val Tyr Ile Val Ala Lys Arg Thr Thr Lys Asn Leu Glu Ala Gly
1 5 10 15

Val Met Lys Glu Met Ser Asn Ser Lys Glu Leu Thr Leu Arg Ile His
20 25 30

Ser Lys Asn Phe His Glu Asp Thr Leu Ser Ser Thr Lys Ala Lys Gly
35 40 45

His Asn Pro Arg Ser Ser Ile Ala Val Lys Leu Phe Lys Phe Ser Arg
50 55 60

Glu Lys Lys Ala Xaa Lys Thr Leu
65 70

<210> 7
<211> 22
<212> PRT
<213> Homo Sapien

<400> 7

Cys Leu Asp Gly Leu Thr Thr Cys Gly Val Val Tyr Pro Leu Ser Lys
1 5 10 15

Asn His Leu Val Val Leu
20

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<211> 29
<212> PRT
<213> Homo Sapien

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Cys Arg Ile Val Cys Arg His Ala Gln Gln Ile Ala Leu Gln Arg His
1 5 10 15

Leu Leu Pro Ala Ser His Tyr Val Ala Thr Arg Lys Gly
20 25

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<212> PRT
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Lys Ile Ile Lys Arg
20

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<213> Homo Sapien

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Lys Ile Ile Lys Arg
20

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Val Thr Ile Leu
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<210> 12

<211> 9
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Ala Leu Ile Thr Arg Thr Val Lys Lys
1 5

<210> 13
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1 5 10 15
Thr Leu Thr Val Ile Thr Leu Glu
20

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<212> PRT
<213> Homo Sapien

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Ile Leu Leu Val Leu Phe Tyr Pro Leu Asn Ser Tyr Ala Asn Pro Phe
1 5 10 15
Leu Tyr Ala Ile Phe Thr Lys Ala
20

<210> 15
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<212> PRT
<213> Homo Sapien

<220>
<223> Xaa is normally either Glu or Asp.

<400> 15
Xaa Arg Tyr
1

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<400> 16
Glu Lys Lys Ala Ala
1 5

<210> 17
<211> 5
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<213> Homo Sapien

<220>
<223> First Xaa can be any amino acid, preferably Gly,
Ala, or Lys.

<220>
<223> Second and third Xaa denote a basic amino acid.

<220>
<223> Fourth Xaa denotes a hydrophobic amino acid.

<220>
<223> Fifth Xaa denotes any amino acid, preferably Lys,
Arg, Glu, or a hydrophobic amino acid with a
differing side chain to the original hydrophobic
amino acid in that position.

<400> 17
Xaa Xaa Xaa Xaa Xaa
1 5

<210> 18
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<212> PRT
<213> Homo Sapien

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<223> Xaa is Glu, Asp, Gln, His or Lys.

<400> 18
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Val Val Ala Ala Val Thr Leu Cys
20

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<213> Homo Sapien

<400> 19
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1 5 10 15

Leu Val Val Val Val Gly Ile Leu Ile
20 25

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Gln Leu Pro Tyr
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ctggctctgc actttgctgc 20

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agcatcacat aggtccgtgt cac 23

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accagaaagg gtgtgggtac actg 24

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ggaacgaaag gcactttgg 19

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gctgcctcgg gattatttag 20

<210> 26
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<400> 26

gcctattagc aggaacatgg gtg

23

<210> 27

<211> 330

<212> PRT

<213> Homo Sapien

<400> 27

Met Met Trp Gly Ala Gly Ser Pro Leu Ala Trp Leu Ser Ala Gly Ser
1 5 10 15

Gly Asn Val Asn Val Ser Ser Val Gly Pro Ala Glu Gly Pro Thr Gly
20 25 30

Pro Ala Ala Pro Leu Pro Ser Pro Lys Ala Trp Asp Val Val Leu Cys
35 40 45

Ile Ser Gly Thr Leu Val Ser Cys Glu Asn Ala Leu Val Val Ala Ile
50 55 60

Ile Val Gly Thr Pro Ala Phe Arg Ala Pro Met Phe Leu Leu Val Gly
65 70 75 80

Ser Leu Ala Val Ala Asp Leu Leu Ala Gly Leu Gly Leu Val Leu His
85 90 95

Phe Ala Ala Val Phe Cys Ile Gly Ser Ala Glu Met Ser Leu Val Leu
100 105 110

Val Gly Val Leu Ala Met Ala Phe Thr Ala Ser Ile Gly Ser Leu Leu
115 120 125

Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Asn Ala Leu Thr Tyr
130 135 140

Tyr Ser Glu Thr Thr Val Thr Arg Thr Tyr Val Met Leu Ala Leu Val
145 150 155 160

Trp Gly Gly Ala Leu Gly Leu Gly Leu Leu Pro Val Leu Ala Trp Asn
165 170 175

Cys Leu Asp Gly Leu Thr Thr Cys Gly Val Val Tyr Pro Leu Ser Lys
180 185 190

Asn His Leu Val Val Leu Ala Ile Ala Phe Phe Met Val Phe Gly Ile
195 200 205

Met Leu Gln Leu Tyr Ala Gln Ile Cys Arg Ile Val Cys Arg His Ala
210 215 220

Gln Gln Ile Ala Leu Gln Arg His Leu Leu Pro Ala Ser His Tyr Val
225 230 235 240

Ala Thr Arg Lys Gly Ile Ala Thr Leu Ala Val Val Leu Gly Ala Phe
245 250 255

Ala Ala Cys Trp Leu Pro Phe Thr Val Tyr Cys Leu Leu Gly Asp Ala
260 265 270

His Ser Pro Pro Leu Tyr Thr Tyr Leu Thr Leu Leu Pro Ala Thr Tyr
275 280 285

Asn Ser Met Ile Asn Pro Ile Ile Tyr Ala Phe Arg Asn Gln Asp Val
290 295 300

Gln Lys Val Leu Trp Ala Val Cys Cys Cys Cys Ser Ser Ser Lys Ile
305 310 315 320

Pro Phe Arg Ser Arg Ser Pro Ser Asp Val
325 330

<210> 28
<211> 362
<212> PRT
<213> Homo Sapien

<400> 28
Met Asn Ala Ser Ala Ala Ser Leu Asn Asp Ser Gln Val Val Val Val
1 5 10 15

Ala Ala Glu Gly Ala Ala Ala Ala Thr Ala Ala Gly Gly Pro Asp
20 25 30

Thr Gly Glu Trp Gly Pro Pro Ala Ala Ala Ala Leu Gly Ala Gly Gly
35 40 45

Gly Ala Asn Gly Ser Leu Glu Leu Ser Ser Gln Leu Ser Ala Gly Pro
50 55 60

Pro Gly Leu Leu Leu Pro Ala Val Asn Pro Trp Asp Val Leu Leu Cys
65 70 75 80

Val Ser Gly Thr Val Ile Ala Gly Glu Asn Ala Leu Val Val Ala Leu
85 90 95

Ile Ala Ser Thr Pro Ala Leu Arg Thr Pro Met Phe Val Leu Val Gly
100 105 110

Ser Leu Ala Thr Ala Asp Leu Leu Ala Gly Cys Gly Leu Ile Leu His
115 120 125

Phe Val Phe Gln Tyr Leu Val Pro Ser Glu Thr Val Ser Leu Leu Thr
130 135 140

Val Gly Phe Leu Val Ala Ser Phe Ala Ala Ser Val Ser Ser Leu Leu
145 150 155 160

Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Asn Ala Leu Thr Tyr
165 170 175

Tyr Ser Arg Arg Thr Leu Leu Gly Val His Leu Leu Leu Ala Ala Thr
 180 185 190
 Trp Thr Val Ser Leu Gly Leu Gly Leu Leu Pro Val Leu Gly Trp Asn
 195 200 205
 Cys Leu Ala Glu Arg Ala Ala Cys Ser Val Val Arg Pro Leu Ala Arg
 210 215 220
 Ser His Val Ala Leu Leu Ser Ala Ala Phe Phe Met Val Phe Gly Ile
 225 230 235 240
 Met Leu His Leu Tyr Val Arg Ile Cys Gln Val Val Trp Arg His Ala
 245 250 255
 His Gln Ile Ala Leu Gln Gln His Cys Leu Ala Pro Pro His Leu Ala
 260 265 270
 Ala Thr Arg Lys Gly Val Gly Thr Leu Ala Val Val Leu Gly Thr Phe
 275 280 285
 Gly Ala Ser Trp Leu Pro Phe Ala Ile Tyr Cys Val Val Gly Ser His
 290 295 300
 Glu Asp Pro Ala Val Tyr Thr Tyr Ala Thr Leu Leu Pro Ala Thr Tyr
 305 310 315 320
 Asn Ser Met Ile Asn Pro Ile Ile Tyr Ala Phe Arg Asn Gln Glu Ile
 325 330 335
 Gln Arg Ala Leu Trp Leu Leu Leu Cys Gly Cys Phe Gln Ser Lys Val
 340 345 350
 Pro Phe Arg Ser Arg Ser Pro Ser Glu Val
 355 360

<210> 29
 <211> 334
 <212> PRT
 <213> Homo Sapien

<400> 29
 Met Asn Glu Asp Leu Lys Val Asn Leu Ser Gly Leu Pro Arg Asp Tyr
 1 5 10 15
 Leu Asp Ala Ala Ala Glu Asn Ile Ser Ala Ala Val Ser Ser Arg
 20 25 30
 Val Pro Ala Val Glu Pro Glu Pro Glu Leu Val Val Asn Pro Trp Asp
 35 40 45
 Ile Val Leu Cys Thr Ser Gly Thr Leu Ile Ser Cys Glu Asn Ala Ile
 50 55 60
 Val Val Leu Ile Ile Phe His Asn Pro Ser Leu Arg Ala Pro Met Phe

65	70	75	80
Leu Leu Ile Gly Ser	Leu Ala Leu Ala Asp	Leu Leu Ala Gly Ile Gly	
85	90	95	
Leu Ile Thr Asn Phe Val Phe Ala Tyr Leu Leu Gln Ser Glu Ala Thr			
100	105	110	
Lys Leu Val Thr Ile Gly Leu Ile Val Ala Ser Phe Ser Ala Ser Val			
115	120	125	
Cys Ser Leu Leu Ala Ile Thr Val Asp Arg Tyr Leu Ser Leu Tyr Tyr			
130	135	140	
Ala Leu Thr Tyr His Ser Glu Arg Thr Val Thr Phe Thr Tyr Val Met			
145	150	155	160
Leu Val Met Leu Trp Gly Thr Ser Ile Cys Leu Gly Leu Leu Pro Val			
165	170	175	
Met Gly Trp Asn Cys Leu Arg Asp Glu Ser Thr Cys Ser Val Val Arg			
180	185	190	
Pro Leu Thr Lys Asn Asn Ala Ala Ile Leu Ser Val Ser Phe Leu Phe			
195	200	205	
Met Phe Ala Leu Met Leu Gln Leu Tyr Ile Gln Ile Cys Lys Ile Val			
210	215	220	
Met Arg His Ala His Gln Ile Ala Leu Gln His His Phe Leu Ala Thr			
225	230	235	240
Ser His Tyr Val Thr Thr Arg Lys Gly Val Ser Thr Leu Ala Ile Ile			
245	250	255	
Leu Gly Thr Phe Ala Ala Cys Trp Met Pro Phe Thr Leu Tyr Ser Leu			
260	265	270	
Ile Ala Asp Tyr Thr Tyr Pro Ser Ile Tyr Thr Tyr Ala Thr Leu Leu			
275	280	285	
Pro Ala Thr Tyr Asn Ser Ile Ile Asn Pro Val Ile Tyr Ala Phe Arg			
290	295	300	
Asn Gln Glu Ile Gln Lys Ala Leu Cys Leu Ile Cys Cys Gly Cys Ile			
305	310	315	320
Pro Ser Ser Leu Ala Gln Arg Ala Arg Ser Pro Ser Asp Val			
325	330		